

# REPLACEMENT SHEET

## FIG. 1

1	MASTTPITME	DLQKALEAQS	RALRAGLAAG	ASQSRPRPP	RHARLQHLPE	50
51	MTPAVTPEGP	APPRTGANQR	KDWSRAPPPP	EERQESRSQT	PAPKPSRAPP	100
101	QOPOPPRMOT	GRGGSAPRPE	LGPPTNPFQA	AVARGLRPPL	HOPDTEAPTE	150
151	ACVTSWLWSE	GEGAVFYRVD	LHFINLGTPP	LDGEDGRMDPA	LMYNPCGPEP	200
201	PAHVVRAYNQ	PAGDVRGVNG	KGERTYAEQD	FRVGGTRWHR	LLRMPVRGLD	250
251	GDTAPLPPHT	TERIETRSAR	HPWRIRFGAP	OAFLAGLLLA	AVAVGTARAG	300
301	LQPRADMAAP	PMPPQPPRAH	GQHYGHHHHQ	LPFLGHDGHH	GGTLRVGQHH	350
351	RNASDVLPGH	WLQGGWGCYN	LSDYHQGTHV	CHTKHMDFWC	VEHDRPPPAT	400
401	PTSLTTAANY	IAAATPATAP	PPCHAGLNDS	CGGFLSGCGP	MRLPTALTPG	450
451	AVGDLRAVHH	RPVPAYPVCC	AMRWGLPPWE	LVILTARPED	GWTCRGVPAH	500
501	PGTRCELVYS	PMGRATCSPA	SALWLATANA	LSLDHAFAAF	VLLVPWVLIF	550
551	MVCRRACRRP	APPPSPQSS	CRGTTTPAYG	EEAFTYLCTA	PGCATOTVPV	600
601	VRLAGVGFES	KIVDGGCFAP	WDLEATGACI	CEIPTDVSCE	GLGAMYPTAP	650
651	CARIWNGTOR	ACTFWAVNAY	SSGGYAOLAS	YFNPGGSYK	OYHTACEVE	700
701	PAFGHSDAAC	WGFPTDTVMS	VFALASYVOH	PHKTVRVKFH	TETRTVMOLS	750
751	VAGVSCNYTT	EHPFCNTPHG	QLEVQVPPDP	GOLVEYIMNY	TGNQQSRWGL	800
801	GSPNCHGPDY	ASPYCQRHSP	DCSRLVGATP	ERPRLRLVDA	DDPLLRTAPG	850
851	PGEVWYTPVI	GSQARKCGLH	IRAGPYGHAT	YEMPEWIAH	TTSDPMHPPG	900
901	PLGLXFKTVR	PVALPRALAP	PRNVRVTGCV	QCGTPALVEG	LAPGGGNCHL	950
951	TVNGEDVGAF	PPGKFVTAAL	LNTPPPYQVS	CGGESDRASA	GH.....	1000

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FIG. 3

	10	20	30	40	50	
1	MGARASVLSG	GELDRWEKIR	LRPGGKKKYK	LKHIVNASRE	LERFAVNPGL	50
	60	70	80	90	100	
51	LETSEGCRQI	LGQLQPSLQT	GSEELRSLYN	TVATLYCVHQ	RIEIKDTKEA	100
	110	120	130	140	150	
101	LDKIEEEQNK	SKKKAQAAAA	DTGHSSQVSQ	NYPIVQNIQG	QMVHQAI <del>SPR</del>	150
	160	170	180	190	200	
151	TLNAWVKVVE	EKA <del>F</del> SP <del>E</del> VIP	MFSALSEGAT	PQDLN <del>T</del> MLNT	VGGHQAAMQM	200
	210	220	230	240	250	
201	LKETINEEAA	EWDRVHPVHA	GPIAPGQMRE	PRGSDIAGTT	STLQE <del>Q</del> IGWM	250
	260	270	280	290	300	
251	TNNPPIPVGE	IYKRWIILGL	NKIVRMYSPT	SILDIRQGPK	EPFRDYVDRF	300
	310	320	330	340	350	
301	YKTLRAEQAS	QEVKNYMTET	LLVQ <del>N</del> ANPDC	KTILKALGPA	ATLEEMMTAC	350
	360	370	380	390	400	
351	QGVGGPGHKA	RVLA <del>E</del> AMSQV	TNTATIM <del>M</del> QR	GNFRNQRKMV	KCFNCGKEGH	400
	410	420	430	440	450	
401	TARNCRAPRK	KGCNKCGKEG	HQMKDCTERQ	ANFLGKICLP	TREGQGIFFR	450
	460	470	480	490	500	
451	ADQSQQPHHF	FRADQSQQPH	QKRASGLG..	.....	.....	500

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## FIG. 4

	10	20	30	40	50	
1	MRVKEKYQHL	WRNGWKWGTM	LLGILMICS	TEKLWYTVYY	GVPVWKEATT	50
	60	70	80	90	100	
51	TLFCASDAKA	YDEVHNVYA	THACVPTDPN	PQEVVLNVVT	ENFNMWKNOM	100
	110	120	130	140	150	
101	VEQMHEDIIS	LWDQSLKPCV	KLTPLCVSLK	CTDLGNATNT	NSSNTNSSSG	150
	160	170	180	190	200	
151	EMMMEKGEIK	NCSFNISTSI	RGKVQKEYAF	FYKLDIIPID	NOTTSYTLTS	200
	210	220	230	240	250	
201	CNTSVITQAC	PKVSFEPIPI	HYCAPAGFAI	LKCNNKTFNG	TGPCTNVSTV	250
	260	270	280	290	300	
251	QCTHGIRPVV	STQLLNGSL	AEEVVIRSA	NFTDNAKTII	VQLNQSVEIN	300
	310	320	330	340	350	
301	CTRPNNNTRK	SIRIQRGPGR	AFVTIGKIGN	MRQAHCHISR	AKWNATLKQI	350
	360	370	380	390	400	
351	ASKLREQFGN	NKTIIFKQSS	GGDPEIVTHS	FNCGGEFFYC	NSTQLFNSTM	400
	410	420	430	440	450	
401	FNSTWSTEGS	NNTEGSDTIT	LPCRIRQFIN	MWQEVGKAMY	APPISGQIRC	450
	460	470	480	490	500	
451	SSNITGLLLT	ROGGNNNNGS	EIFRPGGGDM	RONWRSELYK	YKVVKIEPLG	500
	510	520	530	540	550	
501	VAPTKAKRRV	VQREKRAVGI	GALFLGFLGA	AGSTMGARSM	TLTVQARQLL	550
	560	570	580	590	600	
551	SGIVQQQNNL	LRAIEAQQHL	LQLTVWGIKQ	LQARILAVER	YKDDQQLLGI	600
	610	620	630	640	650	
601	WGCSGKLICT	TAVPWNASWS	NKSLEQIWN	MTWMEWDREI	NNYTSLIHSL	650
	660	670	680	690	700	
651	IEESQ <sup>u</sup> QQEK	NEQELLELDK	WASLWYWFNI	TNWLWYIKIF	IMIVGGLVGL	700
	710	720	730	740	750	
701	RIVFAVLSIV	NRVRQGYSP	SFQTHLPTPR	GPDRPEGIEE	EGGERDRORS	750
	760	770	780	790	800	
751	IRLVNGSLAL	IWDRLSLCL	FSYHRLRDL	LIVTRIVELL	GRRGWEALKY	800
	810	820	830	840	850	
801	WYNLLQYWSQ	ELKNSAVSLL	NATAIAVAEG	TDRVIEVVQG	ACRAIRHIPR	850
	860	870	880	890	900	
851	RIRQGLERIL	L				900

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## FIG. 5

	10	20	30	40	50	
1	MKTTLKMTAL	AALSAFVLAG	CGSHQMKSEE	HANMQLQQQA	VLGLNWMQDS	50
	60	70	80	90	100	
51	GEYKALAYQA	YNAAKVAFDH	AKVAKGKKKA	VVADLDETML	DNSPYAGWQV	100
	110	120	130	140	150	
101	<u>QNNKP</u> FDGKD	WTRWVDARQS	RAVPGAVEFN	NYVNSHNGKV	FYVTNRKOST	150
	160	170	180	190	200	
151	EKSGTIDDMK	RLGFNGVEES	AFYLKKDKSA	KAARFAEIEK	QGYEIVLYVG	200
	210	220	230	240	250	
201	DNLDDFGNTV	YGKLNADRRR	FVDQNQGKFG	KTFIHLPNAN	YGGWEGGLAE	250
	260	270	280	290	300	
251	GYFKKDTQGQ	IKARLDAVQA	WDGK.....	.....	.....	300

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## FIG. 6

	10	20	30	40	50	
1	<u>IQPPKN</u> LLFS	SLLFSSLLFS	SAAQAASEDR	RSPYYVQAOL	AYAAERITHD	50
	60	70	80	90	100	
51	YPQATGANNT	STVSOYFRNI	RAHSIHPRVS	VGYDFGGWRI	AADYASYRKW	100
	110	120	130	140	150	
101	NNNKYSVNTK	ELENKHNNKK	DLKTENQENG	TFHAASSLGL	SAIYDFKLKG	150
	160	170	180	190	200	
151	KFKPYIGARV	AYGHRHSID	.....	.....	.....	200

## FIG. 9

	10	20	30	40	50	
1	MKVSAAALLCL	LLIAATFIPQ	GLAQPDAINA	PVTCCYNFTN	RKISVQRLAS	50
	60	70	80	90	100	
51	YRRITSSKCP	KEAVIFKTIV	AKEICADPKQ	KWVQDSMDHL	<u>DKQTQTPKT</u>	100

## FIG. 10

	10	20	30	40	50	
1	KSTTCCYRFI	NKKIPKQRLE	SYRRTTSSHC	PREAVIFKDK	EICADPTQKW	50
	60	70	80	90	100	
51	VQDFMKHLDK	<u>KTQTPKL</u>	.....	.....	.....	100

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## FIG. 7

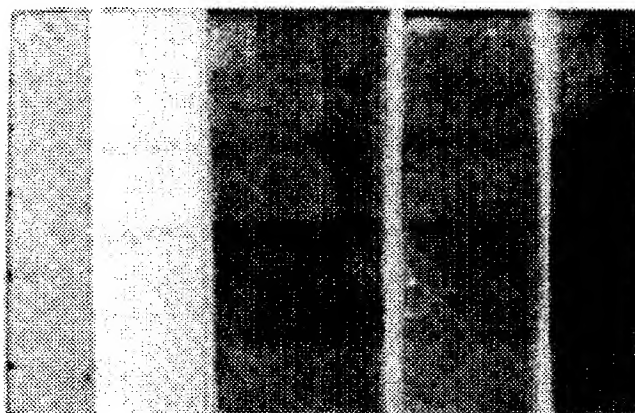
			-11	-1	
			.....	.....	
			....KLMI*K		6
	10	20	30	40	50
7	FVTKM*YKTL	DKYLRRRLIL	NISIV*K*LS	EKR*I*MNKK	KMILTSLASV
	60	70	80	90	100
57	AILGAGFVAS	QPTVVRAEES	PVASQSKAEK	DYDAAKKDAK	NAKKAVEDAQ
	110	120	130	140	150
107	KALDDAKAAQ	KKYDEDQKKT	EEKAALEKAA	SEEMDKAVAA	VQQAYLAYQQ
	160	170	180	190	200
157	ATDKAAKDAA	OKMIDEAKKR	EEEAKTKFNT	VRAMVYPEPE	QLAETKKKSE
	210	220	230	240	250
207	EAKQKAPELT	KKLEEAKAKL	EEAEKKATEA	KQKYDAEEVA	PQAKIAELEN
	260	270	280	290	300
257	QVHRLEQELK	EIDSESEEDY	AKEGFRAPLQ	SKLDAKKAKL	SKLEELSOKI
	310	320	330	340	350
307	DELDAEIAKL	EDQLKAAEEN	NNVEDYFKEG	LEKTIAAKKA	ELEKTEADLK
	360	370	380	390	400
357	KAVNEPEKPA	PAPETPAPEA	PAEQPKPAPA	PQPAPAPKPE	KPAEQPKPEK
	410	420	430	440	450
407	TDDQQAEEEDY	ARRSEEEYNR	LTQQQPPKAE	KPAPAPKTGM	KQENGMYFY
	460	470	480	490	500
457	NTDGSMATGM	LQNGSWYYL	NSNGAMATGM	LQYNGSWYYL	NANGAMATGM
	510	520	530	540	550
507	AKVNGSWYYL	NANGAMATGM	LQYNGSWYYL	NANGAMATGM	AKVNGSWYYL
	560	570	580	590	600
557	NANGAMATGM	LQYNGSWYYL	NANGAMATGM	AKVNGSWYYL	NANGAMATGM
	610	620	630	640	650
607	VKOGDTWYYL	EASGAMKASQ	WFKVSDKWYY	VNGLGALAVN	TTVDGYKYNA
	660	670	680	690	700
657	NGEMV*AD*I	KAC*EHLTF*	F*NKDKVRLN	RFMFVFFRY.	.....
					706

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## FIG. 8

	10	20	30	40	50	
1	MNMKKATIAA	TAGIAVTAFR	APTIRSASTV	VVEAGDTLWG	IAQSKGTTVD	50
	60	70	80	90	100	
51	AIKKANNLTT	DKIVPGQKLQ	VNNEVAAAEK	TEKSVSATYL	NVRSGAGVDN	100
	110	120	130	140	150	
101	SIITSIKGGT	KVTVETTESN	GMHKITYNDG	KTGFVNGKYL	TDKAVSTPVA	150
	160	170	180	190	200	
151	<u>PTQEVKKETT</u>	TQQAAPAAET	KTEVKQTTQA	<u>ITPAPKVAET</u>	KETPVVDQNA	200
	210	220	230	240	250	
201	TTHAVKSGDT	IWALSVKYGV	SVQDIMSNNN	LSSSSIYVGQ	KLAIKQTANT	250
	260	270	280	290	300	
251	<u>ATPKAEVKTE</u>	APAAEKQAAP	VVKENTNTNT	ATTEKKETAT	<u>QQQTAPKAPT</u>	300
	310	320	330	340	350	
301	EAAKPAPAPS	TNTNANKTNT	NTNTNTNTNN	TNTNTPSKNT	NTNSNTNTNT	350
	360	370	380	390	400	
351	NSNTNANQGS	SNNNSNSSAS	AIIAEAQKHL	GKAYSNGGNG	PTTFDCSGYT	400
	410	420	430	440	450	
401	KYVFAKAGIS	LPRTSGAQYA	STTRISEQA	KPGDLVFFDY	GSGISHVGIY	450
	460	470	480	490	500	
451	VGNGQMINAQ	DNGVKYDNIH	GSGNGKYLVG	FGRV.....	.....	500

**FIG. II**



1 2/3 4/5/6 7/8 9/10

Immunoblots of RV antigens reacted with Mab's RV1, RV2, RV3 and RV4. RV antigen: Strain MPV-77 (lot# 50678, Catalogue# EL-05-04) cultured in Vero cells. Purchased from Microbix Biosystems Inc., Toronto, Ontario). All Mab used as tissue culture fluid diluted 1/500.

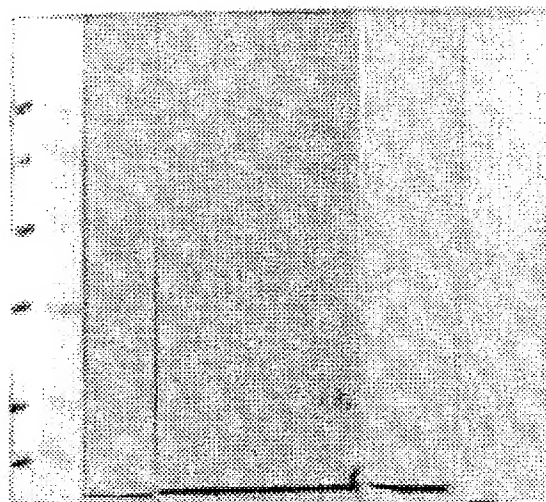
Lane 1 - Molecular weight Markers of 97, 66, 45, 31, 21, and 14 kD.

Lane 2/3 - RV4; Lane 4/5/6 - RV3; Lane 7/8 - RV2; Lane 9/10 - RV1

Lanes 2-9 all illustrate two proteins, 31 kD (major) and 45 kD (minor), identified by reaction with Mab's 1-4



FIG. 12



1 2 3 4/5 6/7

Immunoblots of bacterial antigens reacted with RV Mab RV1.

*H. influenzae* b antigen from ATCC (#10211); *L. monocytogenes* from ATCC (#7644); *S. pneumoniae* from the Caribbean Regional Epidemiology Centre, CAREC, Trinidad; *N. meningitidis* A from ATCC (#13077).

Lane 1 - Molecular weight markers of 97, 66, 45, 31, 21, and 14 kD.

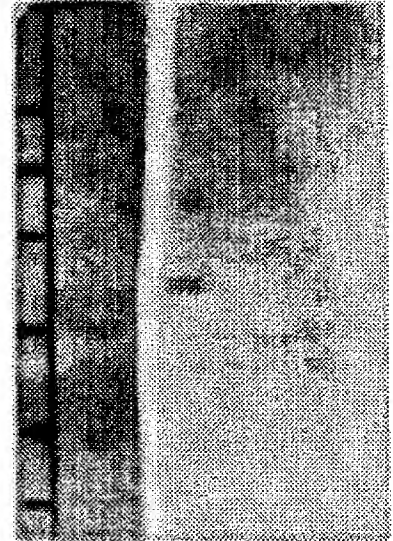
Lane 2 - *H. influenzae* b - proteins of approximate weights of 50, 45, 40, and 25 kD.

Lane 3 - *L. monocytogenes* - proteins of approximate weights of 60 kD (major) and 66 kD (minor).

Lane 4/5 - *S. pneumoniae* - proteins of approximate weights of 60 kD and 66 kD.

Lane 6/7 - *N. meningitidis* - a protein of an approximate weight of 18 kD. All proteins identified by reaction with Mab RV1.

**FIG. 13**



1 2 3/4

Immunoblots of HIV1 antigens reacted with RV Mab RV1.

HTLV-III<sub>B</sub> viral lysate, lot #54-040, purchased from Applied Biotechnologies, Inc., Md., USA.

Lane 1 - Molecular weight markers of 97, 66, 45, 31, 21, and 14 kD.

Lane 2 - Control RV antigens, 31 and 45 kD, reacting with RV1 Mab.

Lane 3/4 - HIV1 proteins of approximate weights of 24 kD and 61 kD, identified by reaction with Mab RV1.